

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
Wen, Zilong
Zhong, Zhong

(ii) TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN SEQUENCES AND METHODS OF USE THEREOF

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/212,185
(B) FILING DATE: 11-MAR-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/980,498
(B) FILING DATE: 23-NOV-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/854,296
(B) FILING DATE: 19-MAR-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO US93/02569
(B) FILING DATE: 19-MAR-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/126,588
(B) FILING DATE: 24-SEP-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-073 CIP

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (vii) IMMEDIATE SOURCE:
 (B) CLONE: HeLa
 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 25..2577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACTGCAACCC	TAATCAGAGC	CCAA	ATG GCG CAG TGG GAA ATG CTG CAG AAT	51
			Met Ala Gln Trp Glu Met Leu Gln Asn	
			1 5	
CTT GAC AGC CCC TTT CAG GAT CAG CTG CAC CAG	CTT TAC TCG CAC AGC			99
Leu Asp Ser Pro Phe Gln Asp Gln Leu His Gln	Leu Tyr Ser His Ser			
10 15	20 25			
CTC CTG CCT GTG GAC ATT CGA CAG TAC TTG GCT GTC	TGG ATT GAA GAC			147
Leu Leu Pro Val Asp Ile Arg Gln Tyr Leu Ala Val	Trp Ile Glu Asp			
30 35	40			
CAG AAC TGG CAG GAA GCT GCA CTT GGG AGT GAT GAT	TCC AAG GCT ACC			195
Gln Asn Trp Gln Glu Ala Ala Leu Gly Ser Asp Asp	Ser Lys Ala Thr			
45 50	55			
ATG CTA TTC TTC CAC TTC TTG GAT CAG CTG AAC TAT	GAG TGT GGC CGT			243
Met Leu Phe Phe His Phe Leu Asp Gln Leu Asn Tyr	Glu Cys Gly Arg			
60 65	70			
TGC AGC CAG GAC CCA GAG TCC TTG TTG CTG CAG CAC	AAT TTG CGG AAA			291
Cys Ser Gln Asp Pro Glu Ser Leu Leu Leu Gln His	Asn Leu Arg Lys			
75 80	85			
TTC TGC CGG GAC ATT CAG CCC TTT TCC CAG GAT CCT	ACC CAG TTG GCT			339
Phe Cys Arg Asp Ile Gln Pro Phe Ser Gln Asp Pro	Thr Gln Leu Ala			
90 95	100 105			
GAG ATG ATC TTT AAC CTC CTT CTG GAA GAA AAA AGA	ATT TTG ATC CAG			387
Glu Met Ile Phe Asn Leu Leu Leu Glu Lys Arg Ile	Leu Ile Gln			
110 115	120			
GCT CAG AGG GCC CAA TTG GAA CAA GGA GAG CCA GTT	CTC GAA ACA CCT			435
Ala Gln Arg Ala Gln Leu Glu Gln Gly Glu Pro Val	Leu Glu Thr Pro			
125 130	135			
GTG GAG AGC CAG CAA CAT GAG ATT GAA TCC CGG ATC	CTG GAT TTA AGG			483
Val Glu Ser Gln Gln His Glu Ile Glu Ser Arg Ile	Leu Asp Leu Arg			
140 145	150			
GCT ATG ATG GAG AAG CTG GTA AAA TCC ATC AGC CAA	CTG AAA GAC CAG			531
Ala Met Met Glu Lys Leu Val Lys, Ser Ile Ser Gln	Leu Lys Asp Gln			
155 160	165			
CAG GAT GTC TTC TGC TTG CGA TAT AAG ATC CAG GCC	AAA GGG AAG ACA			579
Gln Asp Val Phe Cys Phe Arg Tyr Lys Ile Gln Ala	Lys Gly Lys Thr			
170 175	180 185			

CCC TCT CTG GAC CCC CAT CAG ACC AAA GAG CAG AAG ATT CTG CAG GAA Pro Ser Leu Asp Pro His Gln Thr Lys Glu Gln Lys Ile Leu Gln Glu 190 195 200	627
ACT CTC AAT GAA CTG GAC AAA AGG AGA AAG GAG GTG CTG GAT GCC TCC Thr Leu Asn Glu Leu Asp Lys Arg Arg Lys Glu Val Leu Asp Ala Ser 205 210 215	675
AAA GCA CTG CTA CGC CGA TTA ACT ACC CTA ATC GAG CTA CTG CTG CCA Lys Ala Leu Leu Gly Arg Leu Thr Thr Leu Ile Glu Leu Leu Leu Pro 220 225 230	723
AAG TTG GAG GAG TGG AAG GCC CAG CAG CAA AAA GCC TGC ATC AGA GCT Lys Leu Glu Glu Trp Lys Ala Gln Gln Lys Ala Cys Ile Arg Ala 235 240 245	771
CCC ATT GAC CAC GGG TTG GAA CAG CTG GAG ACA TGG TTC ACA GCT GGA Pro Ile Asp His Gly Leu Glu Gln Leu Glu Thr Trp Phe Thr Ala Gly 250 255 260 265	819
GCA AAG CTG TTG TTT CAC CTG AGG CAG CTG CTG AAG GAG CTG AAG GGA Ala Lys Leu Leu Phe His Leu Arg Gln Leu Leu Lys Glu Leu Lys Gly 270 275 280	867
CTG AGT TGC CTG GTT AGC TAT CAG GAT GAC CCT CTG ACC AAA GGG GTG Leu Ser Cys Leu Val Ser Tyr Gln Asp Asp Pro Leu Thr Lys Gly Val 285 290 295	915
GAC CTA CGC AAC GCC CAG GTC ACA GAG TTG CTA CAG CGT CTG CTC CAC Asp Leu Arg Asn Ala Gln Val Thr Glu Leu Leu Gln Arg Leu Leu His 300 305 310	963
AGA GCC TTT GTG GTA GAA ACC CAG CCC TGC ATG CCC CAA ACT CCC CAT Arg Ala Phe Val Val Glu Thr Gln Pro Cys Met Pro Gln Thr Pro His 315 320 325	1011
CGA CCC CTC ATC CTC AAG ACT GGC AGC AAG TTC ACC GTC CGA ACA AGG Arg Pro Leu Ile Leu Lys Thr Gly Ser Lys Phe Thr Val Arg Thr Arg 330 335 340 345	1059
CTG CTG GTG AGA CTC CAG GAA GGC AAT GAG TCA CTG ACT GTG GAA GTC Leu Leu Val Arg Leu Gln Glu Gly Asn Glu Ser Leu Thr Val Glu Val 350 355 360	1107
TCC ATT GAC AGG AAT CCT CCT CAA TTA CAA GGC TTC CGG AAG TTC AAC Ser Ile Asp Arg Asn Pro Pro Gln Leu Gln Gly Phe Arg Lys Phe Asn 365 370 375	1155
ATT CTG ACT TCA AAC CAG AAA ACT TTG ACC CCC GAG AAG GGG CAG AGT Ile Leu Thr Ser Asn Gln Lys Thr Leu Thr Pro Glu Lys Gly Gln Ser 380 385 390	1203
CAG GGT TTG ATT TGG GAC TTT GGT TAC CTG ACT CTG GTG GAG CAA CGT Gln Gly Leu Ile Trp Asp Phe Gly Tyr Leu Thr Leu Val Glu Gln Arg 395 400 405	1251
TCA GGT GGT TCA GGA AAG GGC AGC AAT AAG GGG CCA CTA GGT GTG ACA Ser Gly Gly Ser Gly Lys Gly Ser Asn Lys Gly Pro Leu Gly Val Thr 410 415 420 425	1299
GAG GAA CTG CAC ATC ATC AGC TTC ACG GTC AAA TAT ACC TAC CAG GGT Glu Glu Leu His Ile Ile Ser Phe Thr Val Lys Tyr Thr Tyr Gln Gly 430 435 440	1347
CTG AAG CAG GAG CTG AAA ACG GAC ACC CTC CCT GTG GTG ATT ATT TCC Leu Lys Gln Glu Leu Lys Thr Asp Thr Leu Pro Val Val Ile Ile Ser 445 450 455	1395

AAC ATG AAC CAG CTC TCA ATT GCC TGG GCT TCA GTT CTC TGG TTC AAT Asn Met Asn Gln Leu Ser Ile Ala Trp Ala Ser Val Leu Trp Phe Asn 460 465 470	1443
TTG CTC AGC CCA AAC CTT CAG AAC CAG CAG TTC TTC TCC AAC CCC CCC Leu Leu Ser Pro Asn Leu Gln Asn Gln Phe Phe Ser Asn Pro Pro 475 480 485	1491
AAG GCC CCC TGG AGC TTG CTG GGC CCT GCT CTC AGT TGG CAG TTC TCC Lys Ala Pro Trp Ser Leu Leu Gly Pro Ala Leu Ser Trp Gln Phe Ser 490 495 500 505	1539
TCC TAT GTT GGC CGA GGC CTC AAC TCA GAC CAG CTG AGC ATG CTG AGA Ser Tyr Val Gly Arg Gly Leu Asn Ser Asp Gln Leu Ser Met Leu Arg 510 515 520	1587
AAC AAG CTG TTC GGG CAG AAC TGT AGG ACT GAG GAT CCA TTA TTG TCC Asn Lys Leu Phe Gly Gln Asn Cys Arg Thr Glu Asp Pro Leu Leu Ser 525 530 535	1635
TGG GCT GAC TTC ACT AAG CGA GAG AGC CCT CCT GGC AAG TTA CCA TTC Trp Ala Asp Phe Thr Lys Arg Glu Ser Pro Pro Gly Lys Leu Pro Phe 540 545 550	1683
TGG ACA TGG CTG GAC AAA ATT CTG GAG TTG GTA CAT GAC CAC CTG AAG Trp Thr Trp Leu Asp Lys Ile Leu Glu Leu Val His Asp His Leu Lys 555 560 565	1731
GAT CTC TGG AAT GAT GGA CGC ATC ATG GGC TTT GTG AGT CCG AGC CAG Asp Leu Trp Asn Asp Gly Arg Ile Met Gly Phe Val Ser Arg Ser Gln 570 575 580 585	1779
GAG CGC CGG CTG CTG AAG AAG ACC ATG TCT GGC ACC TTT CTA CTG CGC Glu Arg Arg Leu Leu Lys Lys Thr Met Ser Gly Thr Phe Leu Leu Arg 590 595 600	1827
TTC AGT GAA TCG TCA GAA GGG GGC ATT ACC TGC TCC TGG GTG GAG CAC Phe Ser Glu Ser Ser Glu Gly Gly Ile Thr Cys Ser Trp Val Glu His 605 610 615	1875
CAG GAT GAT GAC AAG GTG CTC ATC TAC TCT GTG CAA CCG TAC ACG AAG Gln Asp Asp Asp Lys Val Leu Ile Tyr Ser Val Gln Pro Tyr Thr Lys 620 625 630	1923
GAG GTG CTG CAG TCA CTC CCG CTG ACT GAA ATC ATC CGC CAT TAC CAG Glu Val Leu Gln Ser Leu Pro Leu Thr Glu Ile Ile Arg His Tyr Gln 635 640 645	1971
TTG CTC ACT GAG GAG AAT ATA CCT GAA AAC CCA CTG CGC TTC CTC TAT Leu Leu Thr Glu Glu Asn Ile Pro Glu Asn Pro Leu Arg Phe Leu Tyr 650 655 660 665	2019
CCC CGA ATC CCC CGG GAT GAA GCT TTT GGG TGC TAC TAC CAG GAG AAA Pro Arg Ile Pro Arg Asp Glu Ala Phe Gly Cys Tyr Tyr Gln Glu Lys 670 675 680	2067
GTT AAT CTC CAG GAA CGG AGG AAA TAC CTG AAA CAC AGG CTC ATT GTG Val Asn Leu Gln Glu Arg Arg Lys Tyr Leu Lys His Arg Leu Ile Val 685 690 695	2115
GTC TCT AAT AGA CAG GTG GAT GAA CTG CAA CAA CCG CTG GAG CTT AAG Val Ser Asn Arg Gln Val Asp Glu Leu Gln Pro Leu Glu Leu Lys 700 705 710	2163
CCA GAG CCA GAG CTG GAG TCA TTA GAG CTG GAA CTA GGG CTG GTG CCA Pro Glu Pro Glu Leu Glu Ser Leu Glu Leu Glu Leu Gly Leu Val Pro 715 720 725	2211

GAG CCA GAG CTC AGC CTG GAC TTA GAG CCA CTG CTG AAG GCA GGG CTG Glu Pro Glu Leu Ser Leu Asp Leu Glu Pro Leu Leu Lys Ala Gly Leu 730 735 740 745	2259
GAT CTG GGG CCA GAG CTA GAG TCT GTG CTG GAG TCC ACT CTG GAG CCT Asp Leu Gly Pro Glu Leu Glu Ser Val Leu Glu Ser Thr Leu Glu Pro 750 755 760	2307
GTG ATA GAG CCC ACA CTA TGC ATG GTA TCA CAA ACA GTG CCA GAG CCA Val Ile Glu Pro Thr Leu Cys Met Val Ser Gln Thr Val Pro Glu Pro 765 770 775	2355
GAC CAA GGA CCT GTA TCA CAG CCA GTG CCA GAG CCA GAT TTG CCC TGT Asp Gln Gly Pro Val Ser Gln Pro Val Pro Glu Pro Asp Leu Pro Cys 780 785 790	2403
GAT CTG AGA CAT TTG AAC ACT GAG CCA ATG GAA ATC TTC AGA AAC TGT Asp Leu Arg His Leu Asn Thr Glu Pro Met Glu Ile Phe Arg Asn Cys 795 800 805	2451
GTA AAG ATT GAA GAA ATC ATG CCG AAT GGT GAC CCA CTG TTG GCT GGC Val Lys Ile Glu Glu Ile Met Pro Asn Gly Asp Pro Leu Leu Ala Gly 810 815 820 825	2499
CAG AAC ACC GTG GAT GAG GTT TAC GTC TCC CGC CCC AGC CAC TTC TAC Gln Asn Thr Val Asp Glu Val Tyr Val Ser Arg Pro Ser His Phe Tyr 830 835 840	2547
ACT GAT GGA CCC TTG ATG CCT TCT GAC TTC TAGGAACCAC ATTTCCCTCTG Thr Asp Gly Pro Leu Met Pro Ser Asp Phe 845 850	2597
TTCTTTCAT ATCTCTTGC CCTTCCTACT CCTCATAGCA TGATATTGTT CTCCAAGGAT	2657
GGGAATCAGG CATGTGTCCTTCC TTCCAAGCTG TGTAACTGT TCAAACCTCAG GCCTGTGTGA	2717
CTCCATTGGG GTGAGAGGTG AAAGCATAAC ATGGGTACAG AGGGGACAAC AATGAATCAG	2777
AACAGATGCT GAGCCATAGG TCTAAATAGG ATCCTGGAGG CTGCCTGCTG TGCTGGAGG	2837
TATAGGGGTC CTGGGGCAG GCCAGGGCAG TTGACAGGTA CTTGGAGGGC TCAGGGCAGT	2897
GGCTCTTTC CAGTATGGAA GGATTTAACAC ATTTTAATAG TTGGTTAGGC TAAACTGGTG	2957
CATACTGGCA TTGGCCTTGG TGGGGAGCAC AGACACAGGA TAGGACTCCA TTTCTTCTT	3017
CCATTCCCTTC ATGTCTAGGA TAACTTGCTT TCTTCTTCC TTTACTCCTG GCTCAAGCCC	3077
TGAATTTCTT CTTTCTCTGC AGGGGTTGAG AGCTTCTGC CTTAGCCTAC CATGTGAAAC	3137
TCTACCCCTGA AGAAAGGGAT GGATAGGAAG TAGACCTCTT TTTCTTACCA GTCTCCTCCC	3197
CTACTCTGCC CCCTAAGCTG GCTGTACCTG TTCCCTCCCCC ATAAAATGAT CCTGCCAATC	3257
TAAAAAAAAA A	3268

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 851 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Gln Trp Glu Met Leu Gln Asn Leu Asp Ser Pro Phe Gln Asp
1 5 10 15

Gln Leu His Gln Leu Tyr Ser His Ser Leu Leu Pro Val Asp Ile Arg
20 25 30

Gln Tyr Leu Ala Val Trp Ile Glu Asp Gln Asn Trp Gln Glu Ala Ala
35 40 45

Leu Gly Ser Asp Asp Ser Lys Ala Thr Met Leu Phe Phe His Phe Leu
50 55 60

Asp Gln Leu Asn Tyr Glu Cys Gly Arg Cys Ser Gln Asp Pro Glu Ser
65 70 75 80

Leu Leu Leu Gln His Asn Leu Arg Lys Phe Cys Arg Asp Ile Gln Pro
85 90 95

Phe Ser Gln Asp Pro Thr Gln Leu Ala Glu Met Ile Phe Asn Leu Leu
100 105 110

Leu Glu Glu Lys Arg Ile Leu Ile Gln Ala Gln Arg Ala Gln Leu Glu
115 120 125

Gln Gly Glu Pro Val Leu Glu Thr Pro Val Glu Ser Gln Gln His Glu
130 135 140

Ile Glu Ser Arg Ile Leu Asp Leu Arg Ala Met Met Glu Lys Leu Val
145 150 155 160

Lys Ser Ile Ser Gln Leu Lys Asp Gln Gln Asp Val Phe Cys Phe Arg
165 170 175

Tyr Lys Ile Gln Ala Lys Gly Lys Thr Pro Ser Leu Asp Pro His Gln
180 185 190

Thr Lys Glu Gln Lys Ile Leu Gln Glu Thr Leu Asn Glu Leu Asp Lys
195 200 205

Arg Arg Lys Glu Val Leu Asp Ala Ser Lys Ala Leu Leu Gly Arg Leu
210 215 220

Thr Thr Leu Ile Glu Leu Leu Leu Pro Lys Leu Glu Glu Trp Lys Ala
225 230 235 240

Gln Gln Gln Lys Ala Cys Ile Arg Ala Pro Ile Asp His Gly Leu Glu
245 250 255

Gln Leu Glu Thr Trp Phe Thr Ala Gly Ala Lys Leu Leu Phe His Leu
260 265 270

Arg Gln Leu Leu Lys Glu Leu Lys Gly Leu Ser Cys Leu Val Ser Tyr
275 280 285

Gln Asp Asp Pro Leu Thr Lys Gly Val Asp Leu Arg Asn Ala Gln Val
290 295 300

Thr Glu Leu Leu Gln Arg Leu Leu His Arg Ala Phe Val Val Glu Thr
305 310 315 320

Gln Pro Cys Met Pro Gln Thr Pro His Arg Pro Leu Ile Leu Lys Thr
325 330 335

Gly Ser Lys Phe Thr Val Arg Thr Arg Leu Leu Val Arg Leu Gln Glu
340 345 350

Gly Asn Glu Ser Leu Thr Val Glu Val Ser Ile Asp Arg Asn Pro Pro
355 360 365

Gln Leu Gln Gly Phe Arg Lys Phe Asn Ile Leu Thr Ser Asn Gln Lys
370 375 380

Thr Leu Thr Pro Glu Lys Gly Gln Ser Gln Gly Leu Ile Trp Asp Phe
385 390 395 400

Gly Tyr Leu Thr Leu Val Glu Gln Arg Ser Gly Gly Ser Gly Lys Gly
405 410 415

Ser Asn Lys Gly Pro Leu Gly Val Thr Glu Glu Leu His Ile Ile Ser
420 425 430

Phe Thr Val Lys Tyr Thr Tyr Gln Gly Leu Lys Gln Glu Leu Lys Thr
435 440 445

Asp Thr Leu Pro Val Val Ile Ile Ser Asn Met Asn Gln Leu Ser Ile
450 455 460

Ala Trp Ala Ser Val Leu Trp Phe Asn Leu Leu Ser Pro Asn Leu Gln
465 470 475 480

Asn Gln Gln Phe Phe Ser Asn Pro Pro Lys Ala Pro Trp Ser Leu Leu
485 490 495

Gly Pro Ala Leu Ser Trp Gln Phe Ser Ser Tyr Val Gly Arg Gly Leu
500 505 510

Asn Ser Asp Gln Leu Ser Met Leu Arg Asn Lys Leu Phe Gly Gln Asn
515 520 525

Cys Arg Thr Glu Asp Pro Leu Leu Ser Trp Ala Asp Phe Thr Lys Arg
530 535 540

Glu Ser Pro Pro Gly Lys Leu Pro Phe Trp Thr Trp Leu Asp Lys Ile
545 550 555 560

Leu Glu Leu Val His Asp His Leu Lys Asp Leu Trp Asn Asp Gly Arg
565 570 575

Ile Met Gly Phe Val Ser Arg Ser Gln Glu Arg Arg Leu Leu Lys Lys
580 585 590

Thr Met Ser Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Glu Gly
595 600 605

Gly Ile Thr Cys Ser Trp Val Glu His Gln Asp Asp Asp Lys Val Leu
610 615 620

Ile Tyr Ser Val Gln Pro Tyr Thr Lys Glu Val Leu Gln Ser Leu Pro
625 630 635 640

Leu Thr Glu Ile Ile Arg His Tyr Gln Leu Leu Thr Glu Glu Asn Ile
645 650 655

Pro Glu Asn Pro Leu Arg Phe Leu Tyr Pro Arg Ile Pro Arg Asp Glu
660 665 670

Ala Phe Gly Cys Tyr Tyr Gln Glu Lys Val Asn Leu Gln Glu Arg Arg
675 680 685

Lys Tyr Leu Lys His Arg Leu Ile Val Val Ser Asn Arg Gln Val Asp
690 695 700

Glu Leu Gln Gln Pro Leu Glu Leu Lys Pro Glu Pro Glu Leu Glu Ser
705 710 715 720

Leu Glu Leu Glu Leu Gly Leu Val Pro Glu Pro Glu Leu Ser Leu Asp
725 730 735

Leu Glu Pro Leu Leu Lys Ala Gly Leu Asp Leu Gly Pro Glu Leu Glu
 740 745 750

Ser Val Leu Glu Ser Thr Leu Glu Pro Val Ile Glu Pro Thr Leu Cys
 755 760 765

Met Val Ser Gln Thr Val Pro Glu Pro Asp Gln Gly Pro Val Ser Gln
 770 775 780

Pro Val Pro Glu Pro Asp Leu Pro Cys Asp Leu Arg His Leu Asn Thr
 785 790 795 800

Glu Pro Met Glu Ile Phe Arg Asn Cys Val Lys Ile Glu Glu Ile Met
 805 810 815

Pro Asn Gly Asp Pro Leu Leu Ala Gly Gln Asn Thr Val Asp Glu Val
 820 825 830

Tyr Val Ser Arg Pro Ser His Phe Tyr Thr Asp Gly Pro Leu Met Pro
 835 840 845

Ser Asp Phe
 850

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3943 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Human Stat91
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 197..2449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATTAACCTC TCGCCGAGCC CCTCCGCAGA CTCTGCGCCG GAAAGTTCA TTTGCTGTAT	60
GCCATCCTCG AGAGCTGTCT AGGTTAACGT TCGCACTCTG TGTATATAAC CTCGACAGTC	120
TTGGCACCTA ACGTGCTGTG CGTAGCTGCT CCTTTGGTTG AATCCCCAGG CCCTTGTG	180
GGCACAAGGT GGCAGG ATG TCT CAG TGG TAC GAA CTT CAG CAG CTT GAC	229
Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp	
1 , , 5 , 10	
TCA AAA TTC CTG GAG CAG GTT CAC CAG CTT TAT GAT GAC AGT TTT CCC	277
Ser Lys Phe Leu Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro	
15 20 25	
ATG GAA ATC AGA CAG TAC CTG GCA CAG TGG TTA GAA AAG CAA GAC TGG	325
Met Glu Ile Arg Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp	
30 35 40	

GAG CAC GCT GCC AAT GAT GTT TCA TTT GCC ACC ATC CGT TTT CAT GAC Glu His Ala Ala Asn Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp 45 50 55	373
CTC CTG TCA CAG CTG GAT CAA TAT AGT CGC TTT TCT TTG GAG AAT Leu Leu Ser Gln Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn 60 65 70 75	421
AAC TTC TTG CTA CAG CAT AAC ATA AGG AAA AGC AAG CGT AAT CTT CAG Asn Phe Leu Leu Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln 80 85 90	469
GAT AAT TTT CAG GAA GAC CCA ATC CAG ATG TCT ATG ATC ATT TAC AGC Asp Asn Phe Gln Glu Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser 95 100 105	517
TGT CTG AAG GAA GAA AGG AAA ATT CTG GAA AAC GCC CAG AGA TTT AAT Cys Leu Lys Glu Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn 110 115 120	565
CAG GCT CAG TCG GGG AAT ATT CAG AGC ACA GTG ATG TTA GAC AAA CAG Gln Ala Gln Ser Gly Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln 125 130 135	613
AAA GAG CTT GAC AGT AAA GTC AGA AAT GTG AAG GAC AAG GTT ATG TGT Lys Glu Leu Asp Ser Lys Val Arg Asn Val Lys Asp Lys Val Met Cys 140 145 150 155	661
ATA GAG CAT GAA ATC AAG AGC CTG GAA GAT TTA CAA GAT GAA TAT GAC Ile Glu His Glu Ile Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp 160 165 170	709
TTC AAA TGC AAA ACC TTG CAG AAC AGA GAA CAC GAG ACC AAT GGT GTG Phe Lys Cys Lys Thr Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val 175 180 185	757
GCA AAG AGT GAT CAG AAA CAA GAA CAG CTG TTA CTC AAG AAG ATG TAT Ala Lys Ser Asp Gln Lys Gln Glu Gln Leu Leu Lys Lys Met Tyr 190 195 200	805
TTA ATG CTT GAC AAT AAG AGA AAG GAA GTA GTT CAC AAA ATA ATA GAG Leu Met Leu Asp Asn Lys Arg Lys Glu Val Val His Lys Ile Ile Glu 205 210 215	853
TTG CTG AAT GTC ACT GAA CTT ACC CAG AAT GCC CTG ATT AAT GAT GAA Leu Leu Asn Val Thr Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu 220 225 230 235	901
CTA GTG GAG TGG AAG CGG AGA CAG CAG AGC GCC TGT ATT GGG GGG CCG Leu Val Glu Trp Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro 240 245 250	949
CCC AAT GCT TGC TTG GAT CAG CTG CAG AAC TGG TTC ACT ATA GTT GCG Pro Asn Ala Cys Leu Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala 255 260 265	997
GAG AGT CTG CAG CAA GTT CGG CAG CAG CTT AAA AAG TTG GAG GAA TTG Glu Ser Leu Gln Gln Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu 270 275 280	1045
GAA CAG AAA TAC ACC TAC GAA CAT GAC CCT ATC ACA AAA AAC AAA CAA Glu Gln Lys Tyr Thr Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln 285 290 295	1093
GTG TTA TGG GAC CGC ACC TTC AGT CTT TTC CAG CAG CTC ATT CAG AGC Val Leu Trp Asp Arg Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser 300 305 310 315	1141

TCG TTT GTG GTG GAA AGA CAG CCC TGC ATG CCA ACG CAC CCT CAG AGG Ser Phe Val Val Glu Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg 320 325 330	1189
CCG CTG GTC TTG AAG ACA GGG GTC CAG TTC ACT GTG AAG TTG AGA CTG Pro Leu Val Leu Lys Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu 335 340 345	1237
TTG GTG AAA TTG CAA GAG CTG AAT TAT AAT TTG AAA GTC AAA GTC TTA Leu Val Lys Leu Gln Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu 350 355 360	1285
TTT GAT AAA GAT GTG AAT GAG AGA AAT ACA GTA AAA GGA TTT AGG AAG Phe Asp Lys Asp Val Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys 365 370 375	1333
TTC AAC ATT TTG GGC ACG CAC ACA AAA GTG ATG AAC ATG GAG GAG TCC Phe Asn Ile Leu Gly Thr His Thr Lys Val Met Asn Met Glu Glu Ser 380 385 390 395	1381
ACC AAT GGC AGT CTG GCG GCT GAA TTT CGG CAC CTG CAA TTG AAA GAA Thr Asn Gly Ser Leu Ala Glu Phe Arg His Leu Gln Leu Lys Glu 400 405 410	1429
CAG AAA AAT GCT GGC ACC AGA ACG AAT GAG GGT CCT CTC ATC GTT ACT Gln Lys Asn Ala Gly Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr 415 420 425	1477
GAA GAG CTT CAC TCC CTT AGT TTT GAA ACC CAA TTG TGC CAG CCT GGT Glu Glu Leu His Ser Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly 430 435 440	1525
TTG GTA ATT GAC CTC GAG ACG ACC TCT CTG CCC GTT GTG GTG ATC TCC Leu Val Ile Asp Leu Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser 445 450 455	1573
AAC GTC AGC CAG CTC CCG AGC GGT TGG GCC TCC ATC CTT TGG TAC AAC Asn Val Ser Gln Leu Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn 460 465 470 475	1621
ATG CTG GTG GCG GAA CCC AGG AAT CTG TCC TTC CTG ACT CCA CCA Met Leu Val Ala Glu Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro 480 485 490	1669
TGT GCA CGA TGG GCT CAG CTT TCA GAA GTG CTG AGT TGG CAG TTT TCT Cys Ala Arg Trp Ala Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser 495 500 505	1717
TCT GTC ACC AAA AGA GGT CTC AAT GTG GAC CAG CTG AAC ATG TTG GGA Ser Val Thr Lys Arg Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly 510 515 520	1765
GAG AAG CTT CTT GGT CCT AAC GCC AGC CCC GAT GGT CTC ATT CCG TGG Glu Lys Leu Leu Gly Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp 525 530 535	1813
ACG AGG TTT TGT AAG GAA AAT ATA AAT GAT AAA AAT TTT CCC TTC TGG Thr Arg Phe Cys Lys Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp 540 545 550 555	1861
CTT TGG ATT GAA AGC ATC CTA GAA CTC ATT AAA AAA CAC CTG CTC CCT Leu Trp Ile Glu Ser Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro 560 565 570	1909
CTC TGG AAT GAT GGG TGC ATC ATG GGC TTC ATC AGC AAG GAG CGA GAG Leu Trp Asn Asp Gly Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu 575 580 585	1957

CGT GCC CTG TTG AAG GAC CAG CAG CCG GGG ACC TTC CTG CTG CGG TTC Arg Ala Leu Leu Lys Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe 590 595 600	2005
AGT GAG AGC TCC CGG GAA GGG GCC ATC ACA TTC ACA TGG GTG GAG CGG Ser Glu Ser Ser Arg Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg 605 610 615	2053
TCC CAG AAC GGA GGC GAA CCT GAC TTC CAT GCG GTT GAA CCC TAC ACG Ser Gln Asn Gly Gly Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr 620 625 630 635	2101
AAG AAA GAA CTT TCT GCT GTT ACT TTC CCT GAC ATC ATT CGC AAT TAC Lys Lys Glu Leu Ser Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr 640 645 650	2149
AAA GTC ATG GCT GCT GAG AAT ATT CCT GAG AAT CCC CTG AAG TAT CTG Lys Val Met Ala Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu 655 660 665	2197
TAT CCA AAT ATT GAC AAA GAC CAT GCC TTT GGA AAG TAT TAC TCC AGG Tyr Pro Asn Ile Asp Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg 670 675 680	2245
CCA AAG GAA GCA CCA GAG CCA ATG GAA CTT GAT GGC CCT AAA GGA ACT Pro Lys Glu Ala Pro Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr 685 690 695	2293
GGA TAT ATC AAG ACT GAG TTG ATT TCT GTG TCT GAA GTT CAC CCT TCT Gly Tyr Ile Lys Thr Glu Leu Ile Ser Val Ser Glu Val His Pro Ser 700 705 710 715	2341
AGA CTT CAG ACC ACA GAC AAC CTG CTC CCC ATG TCT CCT GAG GAG TTT Arg Leu Gln Thr Thr Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe 720 725 730	2389
GAC GAG GTG TCT CGG ATA GTG GGC TCT GTA GAA TTC GAC AGT ATG ATG Asp Glu Val Ser Arg Ile Val Gly Ser Val Glu Phe Asp Ser Met Met 735 740 745	2437
AAC ACA GTA TAGAGCATGA ATTTTTTCA TCTTCTCTGG CGACAGTTT Asn Thr Val 750	2486
CCTTCTCATC TGTGATTCCC TCCTGCTACT CTGTTCTTC ACATCCTGTG TTTCTAGGGA	2546
AATGAAAGAA AGGCCAGCAA ATTGCTGCA ACCTGTTGAT AGCAAGTGAA TTTTTCTCTA	2605
ACTCAGAAC ATCAGTTACT CTGAAGGGCA TCATGCATCT TACTGAAGGT AAAATTGAAA	2666
GGCATTCTCT GAAGAGTGGG TTTCACAAAGT GAAAAACATC CAGATACACC CAAAGTATCA	2726
GGACGAGAAT GAGGGTCCTT TGGGAAAGGA GAAGTTAACG AACATCTAGC AAATGTTATG	2786
CATAAAAGTCA GTGCCAACT GTTATAGGTT GTTGGATAAA TCAGTGGTTA TTTAGGGAAC	2845
TGCTTGACGT AGGAACGGTA AATTCTGTG GGAGAATTCT TACATGTTT CTTTGCTTTA	2905
AGTGTAAC TG GCAGTTTCC ATTGGTTTAC CTGTGAAATA GTTCAAAGCC AAGTTTATAT	2966
ACAATTATAT CAGTCCTCTT TCAAAGGTAG CCATCATGGA TCTGGTAGGG GGAAAATGTG	3026
TATTTTATTA CATCTTTCAC ATTGGCTATT TAAAGACAAA GACAAATTCT GTTCTTGAG	3086
AAGAGAACAT TTCCAAATTCA ACAAGTTGTG TTTGATATCC AAAGCTGAAT ACATTCTGCT	3146
TTCACTCTGG TCACATACAA TTATTTTAC AGTTCTCCCA AGGGAGTTAG GCTATTACAA	3206
ACCACTCATT CAAAAGTTGA AATTAACCAC AGATGTAGAT AAACTCAGAA ATTTAATTCA	3266

TGTTTCTTAA ATGGGCTACT TTGTCCTTT TGTTATTAGG GTGGTATTTA GTCTATTAGC	3326
CACAAAATTG GGAAAGGAGT AGAAAAAGCA GTAACTGACA ACTTGATAAA TACACCAGAG	3386
ATAATATGAG AATCAGATCA TTTCAAAACT CATTCCAT GTAACTGCAT TGAGAACTGC	3446
ATATGTTTCG CTGATATATG TGTTTTCAC ATTTGCGAAT GGTTCCATTC TCTCTCCTGT	3506
ACTTTTCCA GACACTTTTG TGAGTGGATG ATGTTTCGTG AAGTATACTG TATTTTTACC	3566
TTTTCCCTTC CTTATCACTG ACACAAAAAG TAGATTAAGA GATGGGTTTG ACAAGGTTCT	3626
TCCCTTTAAC ATACTGCTGT CTATGTGGCT GTATCTTGTG TTTCCACTAC TGCTACCACA	3686
ACTATATTAT CATGCAAATG CTGTATTCTT CTTGGTGGA GATAAAGATT TCTTGAGTIT	3746
TGTTTTAAAAA TTAAAGCTAA AGTATCTGTA TTGCATTAAA TATAATATCG ACACAGTGCT	3806
TTCCGTGGCA CTGCATACAA TCTGAGGCCT CCTCTCTCAG TTTTATATA GATGGCGAGA	3866
ACCTAAGTTT CAGTTGATT TACAATTGAA ATGACTAAAA AACAAAGAAG ACAACATTAA	3926
AAACAATATT GTTTCTA	3943

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 750 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu Glu	
1 5 10 15	
Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln	
20 25 30	
Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn	
35 40 45	
Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu	
50 55 60	
Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln	
65 70 75 80	
His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu	
85 90 95	
Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu	
100 105 110	
Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly	
115 120 125	
Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser	
130 135 140	
Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile	
145 150 155 160	
Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr	
165 170 175	

Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln
180 185 190

Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn
195 200 205

Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr
210 215 220

Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys
225 230 235 240

Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu
245 250 255

Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln
260 265 270

Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr
275 280 285

Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg
290 295 300

Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu
305 310 315 320

Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys
325 330 335

Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln
340 345 350

Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val
355 360 365

Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly
370 375 380

Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu
385 390 395 400

Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly
405 410 415

Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser
420 425 430

Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu
435 440 445

Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu
450 455 460

Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu
465 470 475 480

Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala
485 490 495

Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg
500 505 510

Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly
515 520 525

Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys
530 535 540

Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser
 545 550 555 560
 Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly
 565 570 575
 Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys
 580 585 590
 Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg
 595 600 605
 Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly
 610 615 620
 Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser
 625 630 635 640
 Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala
 645 650 655
 Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp
 660 665 670
 Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pre Lys Glu Ala Pro
 675 680 685
 Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr
 690 695 700
 Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr Thr
 705 710 715 720
 Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Val Ser Arg
 725 730 735
 Ile Val Gly Ser Val Glu Phe Asp Ser Met Met Asn Thr Val
 740 745 750

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 197..2335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTAAACCTC TCGCCGAGCC CCTCCGCAGA CTCTGCGCCG GAAAGTTCA TTTGCTGTAT	60
GCCATCCTCG AGAGCTGTCT AGGTTAACGT TCGCACTCTG TGTATATAAC CTCGACAGTC	120
TTGGCACCTA ACGTGCTGTG CGTAGCTGCT CCTTTGGTTG AATCCCCAGG CCCTTGTGG	180

GGCACAAAGGT GGCAGG ATG TCT CAG TGG TAC GAA CTT CAG CAG CTT GAC Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp 1 5 10	229
TCA AAA TTC CTG GAG CAG CTT TAT GAT GAC AGT TTT CCC Ser Lys Phe Leu Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro 15 20 25	277
ATG GAA ATC AGA CAG TAC CTG GCA CAG TGG TTA GAA AAG CAA GAC TGG Met Glu Ile Arg Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp 30 35 40	325
GAG CAC GCT GCC AAT GAT GTT TCA TTT GCC ACC ATC CGT TTT CAT GAC Glu His Ala Ala Asn Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp 45 50 55	373
CTC CTG TCA CAG CTG GAT CAA TAT AGT CGC TTT TCT TTG GAG AAT Leu Leu Ser Gln Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn 60 65 70 75	421
AAC TTC TTG CTA CAG CAT AAC ATA AGG AAA AGC AAG CGT AAT CTT CAG Asn Phe Leu Leu Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln 80 85 90	469
GAT AAT TTT CAG GAA GAC CCA ATC CAG ATG TCT ATG ATC ATT TAC AGC Asp Asn Phe Gln Glu Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser 95 100 105	517
TGT CTG AAG GAA GAA AGG AAA ATT CTG GAA AAC GCC CAG AGA TTT AAT Cys Leu Lys Glu Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn 110 115 120	565
CAG GCT CAG TCG GGG AAT ATT CAG AGC ACA GTG ATG TTA GAC AAA CAG Gln Ala Gln Ser Gly Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln 125 130 135	613
AAA GAG CTT GAC AGT AAA GTC AGA AAT GTG AAG GAC AAG GTT ATG TGT Lys Glu Leu Asp Ser Lys Val Arg Asn Val Lys Asp Lys Val Met Cys 140 145 150 155	661
ATA GAG CAT GAA ATC AAG AGC CTG GAA GAT TTA CAA GAT GAA TAT GAC Ile Glu His Glu Ile Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp 160 165 170	709
TTC AAA TGC AAA ACC TTG CAG AAC AGA GAA CAC GAG ACC AAT GGT GTG Phe Lys Cys Lys Thr Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val 175 180 185	757
GCA AAG AGT GAT CAG AAA CAA GAA CAG CTG TTA CTC AAG AAG ATG TAT Ala Lys Ser Asp Gln Lys Gln Glu Gln Leu Leu Lys Lys Met Tyr 190 195 200	805
TTA ATG CTT GAC AAT AAG AGA AAG GAA GTA GTT CAC AAA ATA ATA GAG Leu Met Leu Asp Asn Lys Arg Lys Glu Val Val His Lys Ile Ile Glu 205 210 215	853
TTG CTG AAT GTC ACT GAA CTT ACC CAG AAT GCC CTG ATT AAT GAT GAA Leu Leu Asn Val Thr Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu 220 225 230 235	901
CTA GTG GAG TGG AAG CGG AGA CAG CAG AGC GCC TGT ATT GGG GGG CCG Leu Val Glu Trp Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro 240 245 250	949
CCC AAT GCT TGC TTG GAT CAG CTG CAG AAC TGG TTC ACT ATA GTT GCG Pro Asn Ala Cys Leu Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala 255 260 265	997
GAG AGT CTG CAG CAA GTT CGG CAG CTT AAA AAG TTG GAG GAA TTG	1045

Glu Ser Leu Gln Gln Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu			
270	275	280	
GAA CAG AAA TAC ACC TAC GAA CAT GAC CCT ATC ACA AAA AAC AAA CAA		1093	
Glu Gln Lys Tyr Thr Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln			
285	290	295	
GTG TTA TGG GAC CGC ACC TTC AGT CTT TTC CAG CAG CTC ATT CAG AGC		1141	
Val Leu Trp Asp Arg Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser			
300	305	310	315
TCG TTT GTG GTG GAA AGA CAG CCC TGC ATG CCA ACG CAC CCT CAG AGG		1189	
Ser Phe Val Val Glu Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg			
320	325	330	
CCG CTG GTC TTG AAG ACA GGG GTC CAG TTC ACT GTG AAG TTG AGA CTG		1237	
Pro Leu Val Leu Lys Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu			
335	340	345	
TTG GTG AAA TTG CAA GAG CTG AAT TAT AAT TTG AAA GTC AAA GTC TTA		1285	
Leu Val Lys Leu Gln Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu			
350	355	360	
TTT GAT AAA GAT GTG AAT GAG AGA AAT ACA GTA AAA GGA TTT AGG AAG		1333	
Phe Asp Lys Asp Val Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys			
365	370	375	
TTC AAC ATT TTG GGC ACG CAC ACA AAA GTG ATG AAC ATG GAG GAG TCC		1381	
Phe Asn Ile Leu Gly Thr His Thr Lys Val Met Asn Met Glu Glu Ser			
380	385	390	395
ACC AAT GGC AGT CTG GCG GCT GAA TTT CGG CAC CTG CAA TTG AAA GAA		1429	
Thr Asn Gly Ser Leu Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu			
400	405	410	
CAG AAA AAT GCT GGC ACC AGA ACG AAT GAG GGT CCT CTC ATC GTT ACT		1477	
Gln Lys Asn Ala Gly Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr			
415	420	425	
GAA GAG CTT CAC TCC CTT AGT TTT GAA ACC CAA TTG TGC CAG CCT GGT		1525	
Glu Glu Leu His Ser Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly			
430	435	440	
TTG GTA ATT GAC CTC GAG ACG ACC TCT CTG CCC GTT GTG GTG ATC TCC		1573	
Leu Val Ile Asp Leu Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser			
445	450	455	
AAC GTC AGC CAG CTC CCG AGC GGT TGG GCC TCC ATC CTT TGG TAC AAC		1621	
Asn Val Ser Gln Leu Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn			
460	465	470	475
ATG CTG GTG GCG GAA CCC AGG AAT CTG TCC TTC CTG ACT CCA CCA		1669	
Met Leu Val Ala Glu Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro			
480	485	490	
TGT GCA CGA TGG GCT CAG CTT TCA GAA GTG CTG AGT TGG CAG TTT TCT		1717	
Cys Ala Arg Trp Ala Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser			
495	500	505	
TCT GTC ACC AAA AGA GGT CTC AAT GTG GAC CAG CTG AAC ATG TTG GGA		1765	
Ser Val Thr Lys Arg Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly			
510	515	520	
GAG AAG CTT CTT GGT CCT AAC GCC AGC CCC GAT GGT CTC ATT CCG TGG		1813	
Glu Lys Leu Leu Gly Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp			
525	530	535	

ACG AGG TTT TGT AAG GAA AAT ATA AAT GAT AAA AAT TTT CCC TTC TGG Thr Arg Phe Cys Lys Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp 540 545 550 555	1861
CTT TGG ATT GAA AGC ATC CTA GAA CTC ATT AAA AAA CAC CTG CTC CCT Leu Trp Ile Glu Ser Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro 560 565 570	1909
CTC TGG AAT GAT GGG TGC ATC ATG GGC TTC ATC AGC AAG GAG CGA GAG Leu Trp Asn Asp Gly Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu 575 580 585	1957
CGT GCC CTG TTG AAG GAC CAG CAG CCG GGG ACC TTC CTG CTG CGG TTC Arg Ala Leu Leu Lys Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe 590 595 600	2005
AGT GAG AGC TCC CGG GAA GGG GCC ATC ACA TTC ACA TGG GTG GAG CGG Ser Glu Ser Ser Arg Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg 605 610 615	2053
TCC CAG AAC GGA GGC GAA CCT GAC TTC CAT GCG GTT GAA CCC TAC ACG Ser Gln Asn Gly Gly Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr 620 625 630 635	2101
AAG AAA GAA CTT TCT GCT GTT ACT TTC CCT GAC ATC ATT CGC AAT TAC Lys Lys Glu Leu Ser Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr 640 645 650	2149
AAA GTC ATG GCT GCT GAG AAT ATT CCT GAG AAT CCC CTG AAG TAT CTG Lys Val Met Ala Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu 655 660 665	2197
TAT CCA AAT ATT GAC AAA GAC CAT GCC TTT GGA AAG TAT TAC TCC AGG Tyr Pro Asn Ile Asp Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg 670 675 680	2245
CCA AAG GAA GCA CCA GAG CCA ATG GAA CTT GAT GGC CCT AAA GGA ACT Pro Lys Glu Ala Pro Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr 685 690 695	2293
GGA TAT ATC AAG ACT GAG TTG ATT TCT GTG TCT GAA GTG TAAGTGAACA Gly Tyr Ile Lys Thr Glu Leu Ser Val Ser Glu Val 700 705 710	2342
CAGAAGAGTG ACATGTTTAC AAACCTCAAG CCAGCCTTGC TCCTGGCTGG GGCCTGTTGA	2402
AGATGCTTGT ATTTTACTTT TCCATTGTAA TTGCTATCGC CATCACAGCT GAACTTGTG	2462
AGATCCCCGT GTTACTGCCT ATCAGCATT TACTACTTTA AAAAAAAA AAAAGCAA	2522
AAACCAAATT TGTATTAAAG GTATATAAAT TTTCCAAAAA CTGATACCCT TTGAAAAAGT	2582
ATAAATAAAA TGAGCAAAAG TTGAA	2607

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 712 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu Glu
 1 5 10 15

Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln
20 25 30

Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn
35 40 45

Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu
50 55 60

Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln
65 70 75 80

His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu
85 90 95

Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu
100 105 110

Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly
115 120 125

Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser
130 135 140

Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile
145 150 155 160

Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr
165 170 175

Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln
180 185 190

Lys Gln Glu Gln Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn
195 200 205

Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr
210 215 220

Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys
225 230 235 240

Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu
245 250 255

Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln
260 265 270

Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr
275 280 285

Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg
290 295 300

Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu
305 310 315 320

Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys
325 330 335

Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln
340 345 350

Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val
355 360 365

Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly
370 375 380

Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu
 385 390 395 400
 Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly
 405 410 415
 Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser
 420 425 430
 Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu
 435 440 445
 Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu
 450 455 460
 Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu
 465 470 475 480
 Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala
 485 490 495
 Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg
 500 505 510
 Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly
 515 520 525
 Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys
 530 535 540
 Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser
 545 550 555 560
 Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly
 565 570 575
 Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys
 580 585 590
 Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg
 595 600 605
 Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly
 610 615 620
 Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser
 625 630 635 640
 Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala
 645 650 655
 Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp
 660 665 670
 Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro
 675 680 685
 Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr
 690 695 700
 Glu Leu Ile Ser Val Ser Glu Val,
 705 710

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2277 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mouse

(vii) IMMEDIATE SOURCE:
(B) CLONE: Murine Stat91

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 5..2251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGG ATG TCA CAG TGG TTC GAG CTT CAG CAG CTG GAC TCC AAG TTC CTG Met Ser Gln Trp Phe Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu 1 ..5 10 - 15	49
GAG CAG GTC CAC CAG CTG TAC GAT GAC AGT TTC CCC ATG GAA ATC AGA Glu Gln Val His .Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg 20 25 30	97
CAG TAC CTG GCC CAG TGG CTG GAA AAG CAA GAC TGG GAG CAC GCT GCC Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala 35 40 45	145
TAT GAT GTC TCG TTT GCG ACC ATC CGC TTC CAT GAC CTC CTC TCA CAG Tyr Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln 50 55 60	193
CTG GAC GAC CAG TAC AGC CGC TTT TCT CTG GAG AAT AAT TTC TTG TTG Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu 65 70 75	241
CAG CAC AAC ATA CGG AAA AGC AAG CGT AAT CTC CAG GAT AAC TTC CAA Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln 80 85 90 95	289
GAA GAT CCC GTA CAG ATG TCC ATG ATC ATC TAC AAC TGT CTG AAG GAA Glu Asp Pro Val Gln Met Ser Met Ile Ile Tyr Asn Cys Leu Lys Glu 100 105 110	337
GAA AGG AAG ATT TTG GAA AAT GCC CAA AGA TTT AAT CAG GCC CAG GAG Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Glu 115 120 125	385
GGA AAT ATT CAG AAC ACT GTG ATG TTA GAT AAA CAG AAG iGAG CTG GAC Gly Asn Ile Gln Asn Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp 130 135 140	433
AGT AAA GTC AGA AAT GTG AAG GAT CAA GTC ATG TGC ATA GAG CAG GAA Ser Lys Val Arg Asn Val Lys Asp Gln Val Met Cys Ile Glu Gln Glu 145 150 155	481
ATC AAG ACC CTA GAA GAA TTA CAA GAT GAA TAT GAC TTT AAA TGC AAA Ile Lys Thr Leu Glu Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys 160 165 170 175	529
ACC TCT CAG AAC AGA GAA GGT GAA GCC AAT GGT GTG GCG AAG AGC GAC Thr Ser Gln Asn Arg Glu Gly Glu Ala Asn Gly Val Ala Lys Ser Asp 180 185 190	577

CAA AAA CAG GAA CAG CTG CTG CTC CAC AAG ATG TTT TTA ATG CTT GAC Gln Lys Gln Glu Gln Leu Leu His Lys Met Phe Leu Met Leu Asp 195 200 205	625
AAT AAG AGA AAG GAG ATA ATT CAC AAA ATC AGA GAG TTG CTG AAT TCC Asn Lys Arg Lys Glu Ile Ile His Lys Ile Arg Glu Leu Leu Asn Ser 210 215 220	673
ATC GAG CTC ACT CAG AAC ACT CTG ATT AAT GAC GAG CTC GTG GAG TGG Ile Glu Leu Thr Gln Asn Thr Leu Ile Asn Asp Glu Leu Val Glu Trp 225 230 235	721
AAG CGA AGG CAG CAG AGC GCC TGC ATC GGG GGA CCG CCC AAC GCC TGC Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys 240 245 250 255	769
CTG GAT CAG CTG CAA ACG TGG TTC ACC ATT GTT GCA GAG ACC CTG CAG Leu Asp Gln Leu Gln Thr Trp Phe Thr Ile Val Ala Glu Thr Leu Gln 260 265 270	817
CAG ATC CGT CAG CAG CTT AAA AAG CTG GAG GAG TTG GAA CAG AAA TTC Gln Ile Arg Gln Gln Leu Lys Leu Glu Glu Leu Glu Gln Lys Phe 275 280 285	865
ACC TAT GAG CCC GAC CCT ATT ACA AAA AAC AAG CAG GTG TTG TCA GAT Thr Tyr Glu Pro Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Ser Asp 290 295 300	913
CGA ACC TTC CTC CTC TTC CAG CAG CTC ATT CAG AGC TCC TTC GTG GTA Arg Thr Phe Leu Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val 305 310 315	961
GAA CGA CAG CCG TGC ATG CCC ACT CAC CCG CAG AGG CCC CTG GTC TTG Glu Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu 320 325 330 335	1009
AAG ACT GGG GTA CAG TTC ACT GTC AAG TCG AGA CTG TTG GTG AAA TTG Lys Thr Gly Val Gln Phe Thr Val Lys Ser Arg Leu Leu Val Lys Leu 340 345 350	1057
CAA GAG TCG AAT CTA TTA ACG AAA GTG AAA TGT CAC TTT GAC AAA GAT Gln Glu Ser Asn Leu Leu Thr Lys Val Lys Cys His Phe Asp Lys Asp 355 360 365	1105
GTG AAC GAG AAA AAC ACA GTT AAA GGA TTT CGG AAG TTC AAC ATC TTG Val Asn Glu Lys Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu 370 375 380	1153
GGT ACG CAC ACA AAA GTG ATG AAC ATG GAA GAA TCC ACC AAC GGA AGT Gly Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser 385 390 395	1201
CTG GCA GCT GAG CTC CGA CAC CTG CAA CTG AAG GAA CAG AAA AAC GCT Leu Ala Ala Glu Leu Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala 400 405 410 ; 415	1249
GGG AAC AGA ACT AAT GAG GGG CCT CTC ATT GTC ACC GAA GAA CTT CAC Gly Asn Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His 420 425 430	1297
TCT CTT AGC TTT GAA ACC CAG TTG TGC CAG CCA GGC TTG GTG ATT GAC Ser Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp • 435 440 445	1345
CTG GAG ACC ACC TCT CTT CCT GTC GTG GTG ATC TCC AAC GTC AGC CAG Leu Glu Thr Thr Ser Leu Pro Val Val Ile Ser Asn Val Ser Gln 450 455 460	1393

CTC CCC AGT GGC TGG GCG TCT ATC CTG TGG TAC AAC ATG CTG GTG ACA Leu Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Thr 465 470 475	1441
GAG CCC AGG AAT CTC TCC TTC CTG AAC CCC CCG TGC GCG TGG TGG Glu Pro Arg Asn Leu Ser Phe Phe Leu Asn Pro Pro Cys Ala Trp Trp 480 485 490 495	1489
TCC CAG CTC TCA GAG GTG TTG AGT TGG CAG TTT TCA TCA GTC ACC AAG Ser Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys 500 505 510	1537
AGA GGT CTG AAC GCA GAC CAG CTG AGC ATG CTG GGA GAG AAG CTG CTG Arg Gly Leu Asn Ala Asp Gln Leu Ser Met Leu Gly Glu Lys Leu Leu 515 520 525	1585
GGC CCT AAT GCT GGC CCT GAT GGT CTT ATT CCA TGG ACA AGG TTT TGT Gly Pro Asn Ala Gly Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys 530 535 540	1633
AAG GAA AAT ATT AAT GAT AAA AAT TTC TCC TTC TGG CCT TGG ATT GAC Lys Glu Asn Ile Asn Asp Lys Asn Phe Ser Phe Trp Pro Trp Ile Asp 545 550 555	1681
ACC ATC CTA GAG CTC ATT AAG AAC GAC CTG CTG TGC CTC TGG AAT GAT Thr Ile Leu Glu Leu Ile Lys Asn Asp Leu Leu Cys Leu Trp Asn Asp 560 565 570 575	1729
GGG TGC ATT ATG GGC TTC ATC AGC AAG GAG CGA GAA CGC GCT CTG CTC Gly Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu 580 585 590	1777
AAG GAC CAG CAG CCA GGG ACG TTC CTG CTT AGA TTC AGT GAG AGC TCC Lys Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser 595 600 605	1825
CGG GAA GGG GCC ATC ACA TTC ACA TGG GTG GAA CGG TCC CAG AAC GGA Arg Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly 610 615 620	1873
GGT GAA CCT GAC TTC CAT GCC GTG GAG CCC TAC ACG AAA AAA GAA CTT Gly Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu 625 630 635	1921
TCA GCT GTT ACT TTC CCA GAT ATT ATT CGC AAC TAC AAA GTC ATG GCT Ser Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala 640 645 650 655	1969
GCC GAG AAC ATA CCA GAG AAT CCC CTG AAG TAT CTG TAC CCC AAT ATT Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile 660 665 670	2017
GAC AAA GAC CAC GCC TTT GGG AAG TAT TAT TCC AGA CCA AAG GAA GCA Asp Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala 675 680 685	2065
CCA GAA CCG ATG GAG CTT GAC GAC CCT AAG CGA ACT GGA TAC ATC AAG Pro Glu Pro Met Glu Leu Asp Asp Pro Lys Arg Thr Gly Tyr Ile Lys 690 695 700	2113
ACT GAG TTG ATT TCT GTG TCT GAA GTC CAC CCT TCT AGA CTT CAG ACC Thr Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr 705 710 715	2161
ACA GAC AAC CTG CTT CCC ATG TCT CCA GAG GAG TTT GAT GAG ATG TCC Thr Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Met Ser 720 725 730 735	2209

CGG ATA GTG GGC CCC GAA TTT GAC AGT ATG ATG AGC ACA GTA
Arg Ile Val Gly Pro Glu Phe Asp Ser Met Met Ser Thr Val
740 745

2251

TAAACACGAA TTTCTCTCTG GCGACA

2277

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 749 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Gln Trp Phe Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu Glu
1 5 10 15

Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln
20 25 30

Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Tyr
35 40 45

Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu
50 55 60

Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln
65 70 75 80

His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu
85 90 95

Asp Pro Val Gln Met Ser Met Ile Ile Tyr Asn Cys Leu Lys Glu Glu
100 105 110

Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Glu Gly
115 120 125

Asn Ile Gln Asn Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser
130 135 140

Lys Val Arg Asn Val Lys Asp Gln Val Met Cys Ile Glu Gln Glu Ile
145 150 155 160

Lys Thr Leu Glu Glu Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr
165 170 175

Ser Gln Asn Arg Glu Gly Glu Ala Asn Gly Val Ala Lys Ser Asp Gln
180 185 190

Lys Gln Glu Gln Leu Leu His Lys Met Phe Leu Met Leu Asp Asn
195 200 205

Lys Arg Lys Glu Ile Ile His Lys Ile Arg Glu Leu Leu Asn Ser Ile
210 215 220

Glu Leu Thr Gln Asn Thr Leu Ile Asn Asp Glu Leu Val Glu Trp Lys
225 230 235 240

Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu
245 250 255

Asp Gln Leu Gln Thr Trp Phe Thr Ile Val Ala Glu Thr Leu Gln Gln
260 265 270

Ile Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Phe Thr
275 280 285

Tyr Glu Pro Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Ser Asp Arg
290 295 300

Thr Phe Leu Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu
305 310 315 320

Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys
325 330 335

Thr Gly Val Gln Phe Thr Val Lys Ser Arg Leu Leu Val Lys Leu Gln
340 345 350

Glu Ser Asn Leu Leu Thr Lys Val Lys Cys His Phe Asp Lys Asp Val
355 360 365

Asn Glu Lys Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly
370 375 380

Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu
385 390 395 400

Ala Ala Glu Leu Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly
405 410 415

Asn Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser
420 425 430

Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu
435 440 445

Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu
450 455 460

Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Thr Glu
465 470 475 480

Pro Arg Asn Leu Ser Phe Phe Leu Asn Pro Pro Cys Ala Trp Trp Ser
485 490 495

Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg
500 505 510

Gly Leu Asn Ala Asp Gln Leu Ser Met Leu Gly Glu Lys Leu Leu Gly
515 520 525

Pro Asn Ala Gly Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys
530 535 540

Glu Asn Ile Asn Asp Lys Asn Phe Ser Phe Trp Pro Trp Ile Asp Thr
545 550 555 560

Ile Leu Glu Leu Ile Lys Asn Asp Leu Leu Cys Leu Trp Asn Asp Gly
565 570 575

Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys
580 585 590

Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg
595 600 605

Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly
610 615 620

Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser
625 630 635 640

Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala
 645 650 655
 Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp
 660 665 670
 Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro
 675 680 685
 Glu Pro Met Glu Leu Asp Asp Pro Lys Arg Thr Gly Tyr Ile Lys Thr
 690 695 700
 Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr Thr
 705 710 715 720
 Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Met Ser Arg
 725 730 735
 Ile Val Gly Pro Glu Phe Asp Ser Met Met Ser Thr Val
 740 745

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: -2375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mouse
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: splenic/thymic
 - (B) CLONE: Murine 13sf1
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 34..2277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCCACTACC TGGACGGAGA GAGAGAGAGC AGC ATG TCT CAG TGG AAT CAA GTC	54
Met Ser Gln Trp Asn Gln Val	
1	5
CAA CAA TTA GAA ATC AAG TTT TTG GAG CAA GTA GAT CAG TTC TAT GAT	102
Gln Gln Leu Glu Ile Lys Phe Leu Glu Gln Val Asp Gln Phe Tyr Asp	
10	15
20	
GAC AAC TTT CCT ATG GAA ATC CGG CAT CTG CTA GCT CAG TGG ATT GAG	150
Asp Asn Phe Pro Met Glu Ile Arg His Leu Leu Ala Gln Trp Ile Glu	
25	30
35	
ACT CAA GAC TGG GAA GTA GCT TCT AAC AAT GAA ACT ATG GCA ACA ATT	198
Thr Gln Asp Trp Glu Val Ala Ser Asn Asn Glu Thr Met Ala Thr Ile	
40	45
50	55
CTG CTT CAA AAC TTA CTA ATA CAA TTG GAT GAA CAG TTG GGG CGG GTT	246
Leu Leu Gln Asn Leu Leu Ile Gln Leu Asp Glu Gln Leu Gly Arg Val	
60	65
70	

TCC AAA GAA AAA AAT CTG CTA TTG ATT CAC AAT CTA AAG AGA ATT AGA Ser Lys Glu Lys Asn Leu Leu Leu Ile His Asn Leu Lys Arg Ile Arg	294
75 80 85	
AAA GTT CTT CAG GGC AAG TTT CAT GGA AAT CCA ATG CAT GTA GCT GTG Lys Val Leu Gln Gly Lys Phe His Gly Asn Pro Met His Val Ala Val	342
90 95 100	
GTA ATT TCA AAT TGC TTA AGG GAA GAG AGG AGA ATA TTG GCT GCA GCC Val Ile Ser Asn Cys Leu Arg Glu Arg Arg Ile Leu Ala Ala Ala	390
105 110 115	
AAC ATG CCT ATC CAG GGA CCT CTG GAG AAA TCC TTA CAG AGT TCT TCA Asn Met Pro Ile Gln Gly Pro Leu Glu Lys Ser Leu Gln Ser Ser Ser	438
120 125 130 135	
GTT TCT GAA AGA CAA AGG AAT GTG GAA CAC AAA GTG TCT GCC ATT AAA Val Ser Glu Arg Gln Arg Asn Val Glu His Lys Val Ser Ala Ile Lys	486
140 145 150	
AAC AGT GTG CAG ATG ACA GAA CAA GAT ACC AAA TAC TTA GAA GAC CTG Asn Ser Val Gln Met Thr Glu Gln Asp Thr Lys Tyr Leu Glu Asp Leu	534
155 160 165	
CAA GAT GAG TTT GAC TAC AGG TAT AAA ACA ATT CAG ACA ATG GAT CAG Gln Asp Glu Phe Asp Tyr Arg Tyr Lys Thr Ile Gln Thr Met Asp Gln	582
170 175 180	
GGT GAC AAA AAC AGT ATC CTG GTG AAC CAG GAA GTT TTG ACA CTG CTG Gly Asp Lys Asn Ser Ile Leu Val Asn Gln Glu Val Leu Thr Leu Leu	630
185 190 195	
CAA GAA ATG CTT AAT AGT CTG GAC TTC AAG AGA AAG GAA GCA CTC AGT Gln Glu Met Leu Asn Ser Leu Asp Phe Lys Arg Lys Glu Ala Leu Ser	678
200 205 210 215	
AAG ATG ACG CAG ATA GTG AAC GAG ACA GAC CTG CTC ATG AAC AGC ATG Lys Met Thr Gln Ile Val Asn Glu Thr Asp Leu Leu Met Asn Ser Met	726
220 225 230	
CTT CTA GAA GAG CTG CAG GAC TGG AAA AAG CGG CAC AGG ATT GCC TGC Leu Leu Glu Leu Gln Asp Trp Lys Lys Arg His Arg Ile Ala Cys	774
235 240 245	
ATT GGT GGC CCG CTC CAC AAT GGG CTG GAC CAG CTT CAG AAC TGC TTT Ile Gly Gly Pro Leu His Asn Gly Leu Asp Gln Leu Gln Asn Cys Phe	822
250 255 260	
ACC CTA CTG GCA GAG AGT CTT TTC CAA CTC AGA CAG CAA CTG GAG AAA Thr Leu Leu Ala Glu Ser Leu Phe Gln Leu Arg Gln Gln Leu Glu Lys	870
265 270 275	
CTA CAG GAG CAA TCT ACT AAA ATG ACC TAT GAA GGG GAT CCC ATC CCT Leu Gln Glu Gln Ser Thr Lys Met Thr Tyr Glu Gly Asp Pro Ile Pro	918
280 285 290 295	
GCT CAA AGA GCA CAC CTC CTG GAA AGA GCT ACC TTC CTG ATC TAC AAC Ala Gln Arg Ala His Leu Leu Glu Arg Ala Thr Phe Leu Ile Tyr Asn	966
300 305 310	
CTT TTC AAG AAC TCA TTT GTG GTC GAG CGA CAC GCA TGC ATG CCA ACG Leu Phe Lys Asn Ser Phe Val Val Glu Arg His Ala Cys Met Pro Thr	1014
315 320 325	
CAC CCT CAG AGG CCG ATG GTA CTT AAA ACC CTC ATT CAG TTC ACT GTA His Pro Gln Arg Pro Met Val Leu Lys Thr Leu Ile Gln Phe Thr Val	1062
330 335 340	

DRAFT 2/26/2013

AAA CTG AGA TTA CTA ATA AAA TTG CCG GAA CTA AAC TAT CAG GTG AAA Lys Leu Arg Leu Leu Ile Lys Leu Pro Glu Leu Asn Tyr Gln Val Lys 345 350 355	1110
GTA AAG GCG TCC ATT GAC AAG AAT GTT TCA ACT CTA AGC AAT AGA AGA Val Lys Ala Ser Ile Asp Lys Asn Val Ser Thr Leu Ser Asn Arg Arg 360 365 370 375	1158
TTT GTG CTT TGT GGA ACT CAC GTC AAA GCT ATG TCC AGT GAG GAA TCT Phe Val Leu Cys Gly Thr His Val Lys Ala Met Ser Ser Glu Glu Ser 380 385 390	1206
TCC AAT GGG AGC CTC TCA GTG GAG TTA GAC ATT GCA ACC CAA GGA GAT Ser Asn Gly Ser Leu Ser Val Glu Leu Asp Ile Ala Thr Gln Gly Asp 395 400 405	1254
GAA GTG CAG TAC TGG AGT AAA GGA AAC GAG GGC TGC CAC ATG GTG ACA Glu Val Gln Tyr Trp Ser Lys Gly Asn Glu Gly Cys His Met Val Thr 410 415 420	1302
GAG GAG TTG CAT TCC ATA ACC TTT GAG ACC CAG ATC TGC CTC TAT GGC Glu Glu Leu His Ser Ile Thr Phe Glu Thr Gln Ile Cys Leu Tyr Gly 425 430 435	1350
CTC ACC ATT AAC CTA GAG ACC AGC TCA TTA CCT GPC GTG ATG ATT TCT Leu Thr Ile Asn Leu Glu Thr Ser Ser Leu Pro Val Val Met Ile Ser 440 445 450 455	1398
AAT GTC AGC CAA CTA CCT AAT GCA TGG GCA TCC ATC ATT TGG TAC AAT Asn Val Ser Gln Leu Pro Asn Ala Trp Ala Ser Ile Ile Trp Tyr Asn 460 465 470	1446
GTA TCA ACT AAC GAC TCC CAG AAC TTG GTT TTC TTT AAT AAC CCT CCA Val Ser Thr Asn Asp Ser Gln Asn Leu Val Phe Phe Asn Asn Pro Pro 475 480 485	1494
TCT GTC ACT TTG GGC CAA CTC CTG GAA GTG ATG AGC TGG CAA TTT TCA Ser Val Thr Leu Gly Gln Leu Glu Val Met Ser Trp Gln Phe Ser 490 495 500	1542
TCC TAT GTC GGT CGT GGC CTT AAT TCA GAG CAG CTC AAC ATG CTG GCA Ser Tyr Val Gly Arg Gly Leu Asn Ser Glu Gln Leu Asn Met Leu Ala 505 510 515	1590
GAG AAG CTC ACA GTT CAG TCT AAC TAC AAT GAT GGT CAC CTC ACC TGG Glu Lys Leu Thr Val Gln Ser Asn Tyr Asn Asp Gly His Leu Thr Trp 520 525 530 535	1638
GCC AAG TTC TGC AAG GAA CAT TTG CCT GGC AAA ACA TTT ACC TTC TGG Ala Lys Phe Cys Lys Glu His Leu Pro Gly Lys Thr Phe Thr Phe Trp 540 545 550	1686
ACT TGG CTT GAA GCA ATA TTG GAC CTA ATT AAA AAA CAT ATT CTT CCC Thr Trp Leu Glu Ala Ile Leu Asp Leu Ile Lys Lys His Ile Leu Pro 555 560 565	1734
CTC TGG ATT GAT GGG TAC ATC ATG GGA TTT GTT AGT AAA GAG AAG GAA Leu Trp Ile Asp Gly Tyr Ile Met Gly Phe Val Ser Lys Glu Lys Glu 570 575 580	1782
CGG CTT CTG CTC AAA GAT AAA ATG CCT GGG ACA TTT TTG TTA AGA TTC Arg Leu Leu Leu Lys Asp Lys Met Pro Gly Thr Phe Leu Leu Arg Phe 585 590 595	1830
AGT GAG AGC CAT CTT GGA GGG ATA ACC TTC ACC TGG GTG GAC CAA TCT Ser Glu Ser His Leu Gly Gly Ile Thr Phe Thr Trp Val Asp Gln Ser 600 605 610 615	1878

GAA AAT GGA GAA GTG AGA TTC CAC TCT GTA GAA CCC TAC AAC AAA GGG Glu Asn Gly Glu Val Arg Phe His Ser Val Glu Pro Tyr Asn Lys Gly 620 625 630	1926
AGA CTG TCG GCT CTG GCC TTC GCT GAC ATC CTG CGA GAC TAC AAG GTT Arg Leu Ser Ala Leu Ala Phe Ala Asp Ile Leu Arg Asp Tyr Lys Val 635 640 645	1974
ATC ATG GCT GAA AAC ATC CCT GAA AAC CCT CTG AAG TAC CTC TAC CCT Ile Met Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro 650 655 660	2022
GAC ATT CCC AAA GAC AAA GCC TTT GGC AAA CAC TAC AGC TCC CAG CCG Asp Ile Pro Lys Asp Lys Ala Phe Gly Lys His Tyr Ser Ser Gln Pro 665 670 675	2070
TGC GAA GTC TCA AGA CCA ACC GAA CGG GGA GAC AAG GGT TAC GTC CCC Cys Glu Val Ser Arg Pro Thr Glu Arg Gly Asp Lys Gly Tyr Val Pro 680 685 690 695	2118
TCT GTT TTT ATC CCC ATT TCA ACA ATC CGA AGC GAT TCC ACG GAG CCA Ser Val Phe Ile Pro Ile Ser Thr Ile Arg Ser Asp Ser Thr Glu Pro 700 705 710	2166
CAA TCT CCT TCA GAC CTT CTC CCC ATG TCT CCA AGT GCA TAT GCT GTG Gln Ser Pro Ser Asp Leu Leu Pro Met Ser Pro Ser Ala Tyr Ala Val 715 720 725	2214
CTG AGA GAA AAC CTG AGC CCA ACG ACA ATT GAA ACT GCA ATG AAT TCC Leu Arg Glu Asn Leu Ser Pro Thr Thr Ile Glu Thr Ala Met Asn Ser 730 735 740	2262
CCA TAT TCT GCT GAA TGACGGTGCA AACGGACACT TTAAAGAAGG AAGCAGATGA Pro Tyr Ser Ala Glu 745	2317
AACTGGAGAG TGTTCTTAC CATAGATCAC AATTATTTTC TTCGGCTTTG TAAATACC	2375

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 748 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Gln Trp Asn Gln Val Gln Gln Leu Glu Ile Lys Phe Leu Glu 1 5 10 15
Gln Val Asp Gln Phe Tyr Asp Asn Phe Pro Met Glu Ile Arg His 20 25 30
Leu Leu Ala Gln Trp Ile Glu Thr Gln Asp Trp Glu Val Ala Ser Asn 35 40 45
Asn Glu Thr Met Ala Thr Ile Leu Leu Gln Asn Leu Ile Gln Leu 50 55 60
Asp Glu Gln Leu Gly Arg Val Ser Lys Glu Lys Asn Leu Leu Ile 65 70 75 80
His Asn Leu Lys Arg Ile Arg Lys Val Leu Gln Gly Lys Phe His Gly 85 90 95

C

C

Asn Pro Met His Val Ala Val Val Ile Ser Asn Cys Leu Arg Glu Glu
100 105 110

Arg Arg Ile Leu Ala Ala Ala Asn Met Pro Ile Gln Gly Pro Leu Glu
115 120 125

Lys Ser Leu Gln Ser Ser Ser Val Ser Glu Arg Gln Arg Asn Val Glu
130 135 140

His Lys Val Ser Ala Ile Lys Asn Ser Val Gln Met Thr Glu Gln Asp
145 150 155 160

Thr Lys Tyr Leu Glu Asp Leu Gln Asp Glu Phe Asp Tyr Arg Tyr Lys
165 170 175

Thr Ile Gln Thr Met Asp Gln Gly Asp Lys Asn Ser Ile Leu Val Asn
180 185 190

Gln Glu Val Leu Thr Leu Leu Gln Glu Met Leu Asn Ser Leu Asp Phe
195 200 205

Lys Arg Lys Glu Ala Leu Ser Lys Met Thr Gln Ile Val Asn Glu Thr
210 215 220

Asp Leu Leu Met Asn Ser Met Leu Leu Glu Glu Leu Gln Asp Trp Lys
225 230 235 240

Lys Arg His Arg Ile Ala Cys Ile Gly Gly Pro Leu His Asn Gly Leu
245 250 255

Asp Gln Leu Gln Asn Cys Phe Thr Leu Leu Ala Glu Ser Leu Phe Gln
260 265 270

Leu Arg Gln Gln Leu Glu Lys Leu Gln Glu Gln Ser Thr Lys Met Thr
275 280 285

Tyr Glu Gly Asp Pro Ile Pro Ala Gln Arg Ala His Leu Leu Glu Arg
290 295 300

Ala Thr Phe Leu Ile Tyr Asn Leu Phe Lys Asn Ser Phe Val Val Glu
305 310 315 320

Arg His Ala Cys Met Pro Thr His Pro Gln Arg Pro Met Val Leu Lys
325 330 335

Thr Leu Ile Gln Phe Thr Val Lys Leu Arg Leu Leu Ile Lys Leu Pro
340 345 350

Glu Leu Asn Tyr Gln Val Lys Val Lys Ala Ser Ile Asp Lys Asn Val
355 360 365

Ser Thr Leu Ser Asn Arg Arg Phe Val Leu Cys Gly Thr His Val Lys
370 375 380

Ala Met Ser Ser Glu Glu Ser Ser Asn Gly Ser Leu Ser Val Glu Leu
385 390 395 400

Asp Ile Ala Thr Gln Gly Asp Glu Val Gln Tyr Trp Ser Lys Gly Asn
405 410 415

Glu Gly Cys His Met Val Thr Glu Glu Leu His Ser Ile Thr Phe Glu
420 425 430

Thr Gln Ile Cys Leu Tyr Gly Leu Thr Ile Asn Leu Glu Thr Ser Ser
435 440 445

Leu Pro Val Val Met Ile Ser Asn Val Ser Gln Leu Pro Asn Ala Trp
450 455 460

Ala Ser Ile Ile Trp Tyr Asn Val Ser Thr Asn Asp Ser Gln Asn Leu
 465 470 475 480
 Val Phe Phe Asn Asn Pro Pro Ser Val Thr Leu Gly Gln Leu Leu Glu
 485 490 495
 Val Met Ser Trp Gln Phe Ser Ser Tyr Val Gly Arg Gly Leu Asn Ser
 500 505 510
 Glu Gln Leu Asn Met Leu Ala Glu Lys Leu Thr Val Gln Ser Asn Tyr
 515 520 525
 Asn Asp Gly His Leu Thr Trp Ala Lys Phe Cys Lys Glu His Leu Pro
 530 535 540
 Gly Lys Thr Phe Thr Phe Trp Thr Trp Leu Glu Ala Ile Leu Asp Leu
 545 550 555 560
 Ile Lys Lys His Ile Leu Pro Leu Trp Ile Asp Gly Tyr Ile Met Gly
 565 570 575
 Phe Val Ser Lys Glu Lys Glu Arg Leu Leu Leu Lys Asp Lys Met Pro
 580 585 590
 Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser His Leu Gly Gly Ile Thr
 595 600 605
 Phe Thr Trp Val Asp Gln Ser Glu Asn Gly Glu Val Arg Phe His Ser
 610 615 620
 Val Glu Pro Tyr Asn Lys Gly Arg Leu Ser Ala Leu Ala Phe Ala Asp
 625 630 635 640
 Ile Leu Arg Asp Tyr Lys Val Ile Met Ala Glu Asn Ile Pro Glu Asn
 645 650 655
 Pro Leu Lys Tyr Leu Tyr Pro Asp Ile Pro Lys Asp Lys Ala Phe Gly
 660 665 670
 Lys His Tyr Ser Ser Gln Pro Cys Glu Val Ser Arg Pro Thr Glu Arg
 675 680 685
 Gly Asp Lys Gly Tyr Val Pro Ser Val Phe Ile Pro Ile Ser Thr Ile
 690 695 700
 Arg Ser Asp Ser Thr Glu Pro Gln Ser Pro Ser Asp Leu Leu Pro Met
 705 710 715 720
 Ser Pro Ser Ala Tyr Ala Val Leu Arg Glu Asn Leu Ser Pro Thr Thr
 725 730 735
 Ile Glu Thr Ala Met Asn Ser Pro Tyr Ser Ala Glu
 740 745

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2869 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: splenic/thymic
 (B) CLONE: Murine 19sf6

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 69..2378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCGCGACCA	GCCAGGCCGG	CCAGTCGGGC	TCAGCCCCGA	GACAGTCGAG	ACCCCTGACT	60
GCAGCAGG	ATG GCT CAG TGG AAC CAG	CTG CAG CAG CTG GAC ACA CGC TAC				110
	Met Ala Gln Trp Asn Gln Leu Gln Gln Leu Asp Thr Arg Tyr					
	1	5	10			
CTG AAG CAG CTG CAC CAG	CTG TAC AGC GAC ACG	TTC CCC ATG GAG CTG				158
Leu Lys Gln Leu His Gln Leu Tyr Ser Asp Thr Phe Pro Met Glu Leu						
15	20	25	30			
CGG CAG TTC CTG GCA CCT TGG ATT GAG AGT CAA GAC TGG GCA TAT GCA						206
Arg Gln Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala						
35	40	45				
GCC AGC AAA GAG TCA CAT GCC ACG TTG GTG TTT CAT AAT CTC TTG GGT						254
Ala Ser Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly						
50	55	60				
GAA ATT GAC CAG CAA TAT AGC CGA TTC CTG CAA GAG TCC AAT GTC CTC						302
Glu Ile Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu						
65	70	75				
TAT CAG CAC AAC CTT CGA AGA ATC AAG CAG TTT CTG CAG AGC AGG TAT						350
Tyr Gln His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr						
80	85	90				
CTT GAG AAG CCA ATG GAA ATT GCC CGG ATC GTG GCC CGA TGC CTG TGG						398
Leu Glu Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp						
95	100	105	110			
GAA GAG TCT CGC CTC CTC CAG ACG GCA GCC ACG GCA GCC CAG CAA GGG						446
Glu Glu Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly						
115	120	125				
GGC CAG GCC AAC CAC CCA ACA GCC GCC GTA GTG ACA GAG AAG CAG CAG						494
Gly Gln Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln						
130	135	140				
ATG TTG GAG CAG CAT CTT CAG GAT GTC CGG AAG CGA GTG CAG GAT CTA						542
Met Leu Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu						
145	150	155				
GAA CAG AAA ATG AAG GTG GTG GAG AAC CTC CAG GAC GAC TTT GAT TTC						590
Glu Gln Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe						
160	165	170				
AAC TAC AAA ACC CTC AAG AGC CAA GGA GAC ATG CAG GAT CTG AAT GGA						638
Asn Tyr Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly						
175	180	185	190			
AAC AAC CAG TCT GTG ACC AGA CAG AAG ATG CAG CAG CTG GAA CAG ATG						686
Asn Asn Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met						
195	200	205				

DRAFT 7/26/2002

CTC ACA GCC CTG GAC CAG ATG CGG AGA AGC ATT GTG AGT GAG CTG GCG Leu Thr Ala Leu Asp Gln Met Arg Arg Ser Ile Val Ser Glu Leu Ala 210 215 220	734
GGG CTC TTG TCA GCA ATG GAG TAC GTG CAG AAG ACA CTG ACT GAT GAA Gly Leu Leu Ser Ala Met Glu Tyr Val Gln Lys Thr Leu Thr Asp Glu 225 230 235	782
GAG CTG GCT GAC TGG AAG AGG CGG CCA GAG ATC GCG TGC ATC GGA GGC Glu Leu Ala Asp Trp Lys Arg Arg Pro Glu Ile Ala Cys Ile Gly Gly 240 245 250	830
CCT CCC AAC ATC TGC CTG GAC CGT CTG GAA AAC TGG ATA ACT TCA TTA Pro Pro Asn Ile Cys Leu Asp Arg Leu Glu Asn Trp Ile Thr Ser Leu 255 260 265 270	878
GCA GAA TCT CAA CTT CAG ACC CGC CAA CAA ATT AAG AAA CTG GAG GAG Ala Glu Ser Gln Leu Gln Thr Arg Gln Gln Ile Lys Lys Leu Glu Glu 275 280 285	926
CTG CAG CAG AAA GTG TCC TAC AAG GGC GAC CCT ATC GTG CAG CAC CGG Leu Gln Gln Lys Val Ser Tyr Lys Gly Asp Pro Ile Val Gln His Arg 290 295 300	974
CCC ATG CTG GAG GAG AGG ATC GTG GAG CTG TTC AGA AAC TTA ATG AAG Pro Met Leu Glu Glu Arg Ile Val Glu Leu Phe Arg Asn Leu Met Lys 305 310 315	1022
AGT GCC TTC GTG GTG GAG CGG CAG CCC TGC ATG CCC ATG CAC CCG GAC Ser Ala Phe Val Val Glu Arg Gln Pro Cys Met Pro Met His Pro Asp 320 325 330	1070
CGG CCC TTA GTC ATC AAG ACT GGT GTC CAG TTT ACC ACG AAA GTC AGG Arg Pro Leu Val Ile Lys Thr Gly Val Gln Phe Thr Thr Lys Val Arg 335 340 345 350	1118
TTG CTG GTC AAA TTT CCT GAG TTG AAT TAT CAG CTT AAA ATT AAA GTG Leu Leu Val Lys Phe Pro Glu Leu Asn Tyr Gln Leu Lys Ile Lys Val 355 360 365	1166
TGC ATT GAT AAA GAC TCT GGG GAT GTT GCT GCC CTC AGA GGG TCT CGG Cys Ile Asp Lys Asp Ser Gly Asp Val Ala Ala Leu Arg Gly Ser Arg 370 375 380	1214
AAA TTT AAC ATT CTG GGC ACG AAC ACA AAA GTG ATG AAC ATG GAG GAG Lys Phe Asn Ile Leu Gly Thr Asn Thr Lys Val Met Asn Met Glu Glu 385 390 395	1252
TCT AAC AAC GGC AGC CTG TCT GCA GAG TTC AAG CAC CTG ACC CTT AGG Ser Asn Asn Gly Ser Leu Ser Ala Glu Phe Lys His Leu Thr Leu Arg 400 405 410	1310
GAG CAG AGA TGT GGG AAT GGA GGC CGT GCC AAT TGT GAT GCC TCC TTG Glu Gln Arg Cys Gly Asn Gly Arg Ala Asn Cys Asp Ala Ser Leu 415 420 425 430	1353
ATC GTG ACT GAG GAG CTG CAC CTG ATC ACC TTC GAG ACT GAG GTG TAC Ile Val Thr Glu Glu Leu His Leu Ile Thr Phe Glu Thr Glu Val Tyr 435 440 445	1406
CAC CAA GGC CTC AAG ATT GAC CTA'GAG ACC CAC TCC TTG CCA GTT GTG His Gln Gly Leu Lys Ile Asp Leu Glu Thr His Ser Leu Pro Val Val 450 455 460	1454
GTG ATC TCC AAC ATC TGT CAG ATG CCA AAT GCT TGG GCA TCA ATC CTG Val Ile Ser Asn Ile Cys Gln Met Pro Asn Ala Trp Ala Ser Ile Leu 465 470 475	1502

TGG TAT AAC ATG CTG ACC AAT AAC CCC AAG AAC GTG AAC TTC TTC ACT Trp Tyr Asn Met Leu Thr Asn Asn Pro Lys Asn Val Asn Phe Phe Thr 480 485 490	1550
AAG CCG CCA ATT GGA ACC TGG GAC CAA GTG GCC GAG GTG CTC AGC TGG Lys Pro Pro Ile Gly Thr Trp Asp Gln Val Ala Glu Val Leu Ser Trp 495 500 505 510	1598
CAG TTC TCG TCC ACC ACC AAG CGA GGG CTG AGC ATC GAG CAG CTG ACA Gln Phe Ser Ser Thr Thr Lys Arg Gly Leu Ser Ile Glu Gln Leu Thr 515 520 525	1646
ACG CTG GCT GAG AAG CTC CTA GGG CCT GGT GTG AAC TAC TCA GGG TGT Thr Leu Ala Glu Lys Leu Leu Gly Pro Gly Val Asn Tyr Ser Gly Cys 530 535 540	1694
CAG ATC ACA TGG GCT AAA TTC TGC AAA GAA AAC ATG GCT GGC AAG GGC Gln Ile Thr Trp Ala Lys Phe Cys Lys Glu Asn Met Ala Gly Lys Gly 545 550 555	1742
TTC TCC TTC TGG GTC TGG CTA GAC AAT ATC ATC GAC CTT GTG AAA AAG Phe Ser Phe Trp Val Trp Leu Asp Asn Ile Ile Asp Leu Val Lys Lys 560 565 570	1790
TAT ATC TTG GCC CTT TGG AAT GAA GGG TAC ATC ATG GGT TTC ATC AGC Tyr Ile Leu Ala Leu Trp Asn Glu Gly Tyr Ile Met Gly Phe Ile Ser 575 580 585 590	1838
AAG GAG CGG GAG CGG GCC ATC CTA AGC ACA AAG CCC CCG GGC ACC TTC Lys Glu Arg Glu Arg Ala Ile Leu Ser Thr Lys Pro Pro Gly Thr Phe 595 600 605	1886
CTA CTG CGC TTC AGC GAG AGC AGC AAA GAA GGA GGG GTC ACT TTC ACT Leu Leu Arg Phe Ser Glu Ser Ser Lys Glu Gly Gly Val Thr Phe Thr 610 615 620	1934
TGG GTG GAA AAG GAC ATC AGT GGC AAG ACC CAG ATC CAG TCT GTA GAG Trp Val Glu Lys Asp Ile Ser Gly Lys Thr Gln Ile Gln Ser Val Glu 625 630 635	1982
CCA TAC ACC AAG CAG CAG CTG AAC AAC ATG TCA TTT GCT GAA ATC ATC Pro Tyr Thr Lys Gln Gln Leu Asn Asn Met Ser Phe Ala Glu Ile Ile 640 645 650	2030
ATG GGC TAT AAG ATC ATG GAT GCG ACC AAC ATC CTG GTG TCT CCA CTT Met Gly Tyr Lys Ile Met Asp Ala Thr Asn Ile Leu Val Ser Pro Leu 655 660 665 670	2078
GTC TAC CTC TAC CCC GAC ATT CCC AAG GAG GAG GCA TTT GGA AAG TAC Val Tyr Leu Tyr Pro Asp Ile Pro Lys Glu Glu Ala Phe Gly Lys Tyr 675 680 685	2126
TGT AGG CCC GAG AGC CAG GAG CAC CCC GAA GCC GAC CCA GGT AGT GCT Cys Arg Pro Glu Ser Gln Glu His Pro Glu Ala Asp Pro Gly Ser Ala 690 695 700	2174
GCC CCG TAC CTG AAG ACC AAG TTC ATC TGT GTG ACA CCA ACG ACC TGC Ala Pro Tyr Leu Lys Thr Lys Phe Ile Cys Val Thr Pro Thr Thr Cys 705 710 715	2222
AGC AAT ACC ATT GAC CTG CCG ATG TCC CCC CGC ACT TTA GAT TCA TTG Ser Asn Thr Ile Asp Leu Pro Met Ser Pro Arg Thr Leu Asp Ser Leu 720 725 730	2270
ATG CAG TTT GGA AAT AAC GGT GAA GGT GCT GAG CCC TCA GCA GGA GGG Met Gln Phe Gly Asn Asn Gly Glu Gly Ala Glu Pro Ser Ala Gly Gly 735 740 745 750	2318

CAG TTT GAG TCG CTC ACG TTT GAC ATG GAT CTG ACC TCG GAG TGT GCT Gln Phe Glu Ser Leu Thr Phe Asp Met Asp Leu Thr Ser Glu Cys Ala 755 760 765	2366
ACC TCC CCC ATG TGAGGAGCTG AAACCAGAAG CTGCAGAGAC GTGACTTGAG Thr Ser Pro Met 770	2418
ACACCTGCCCGTGTCCAC CCCTAACAG CCGAACCCCA TATCGTCTGA AACTCCTAAC TTTGTGGITTC CAGATTTTTT TTTTTAATT CCTACTTCTG CTATCTTGG GCAATCTGGG CACTTTAA AAGAGAGAAA TGAGTGAGTG TGGGTGATAA ACTGTTATGT AAAGAGGAGA GACCTCTGAG TCTGGGGATG GGGCTGAGAG CAGAAGGGAG GCAAAGGGGA ACACCTCCTG TCCTGCCCGC CTGCCCTCCT TTTTCAGCAG CTCGGGGTT GGTTGTTAGA CAAGTGCCTC CTGGTGCCCCA TGGCTACCTG TTGCCCCACT CTGTGAGCTG ATACCCCATT CTGGGAACTC CTGGCTCTGC ACTTTCAACC TTGCTAATAT CCACATAGAA GCTAGGACTA AGCCCAGGAG GTTCCCTCTTT AAATTAACAA AAAA AAAAAA A	2478 2538 2598 2658 2718 2778 2838 2869

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 770 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ala Gln Trp Asn Gln Leu Gln Gln Leu Asp Thr Arg Tyr Leu Lys 1 5 10 15
Gln Leu His Gln Leu Tyr Ser Asp Thr Phe Pro Met Glu Leu Arg Gln 20 25 30
Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala Ala Ser 35 40 45
Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly Glu Ile 50 55 60
Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu Tyr Gln 65 70 75 80
His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr Leu Glu 85 90 95
Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp Glu Glu 100 105 110
Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly Gly Gln 115 120 125
Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln Met Leu 130 135 140
Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu Glu Gln 145 150 155 160
Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe Asn Tyr 165 170 175

Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly Asn Asn
180 185 190

Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met Leu Thr
195 200 205

Ala Leu Asp Gln Met Arg Arg Ser Ile Val Ser Glu Leu Ala Gly Leu
210 215 220

Leu Ser Ala Met Glu Tyr Val Gln Lys Thr Leu Thr Asp Glu Glu Leu
225 230 235 240

Ala Asp Trp Lys Arg Arg Pro Glu Ile Ala Cys Ile Gly Gly Pro Pro
245 250 255

Asn Ile Cys Leu Asp Arg Leu Glu Asn Trp Ile Thr Ser Leu Ala Glu
260 265 270

Ser Gln Leu Gln Thr Arg Gln Gln Ile Lys Lys Leu Glu Glu Leu Gln
275 280 285

Gln Lys Val Ser Tyr Lys Gly Asp Pro Ile Val Gln His Arg Pro Met
290 295 300

Leu Glu Glu Arg Ile Val Glu Leu Phe Arg Asn Leu Met Lys Ser Ala
305 310 315 320

Phe Val Val Glu Arg Gln Pro Cys Met Pro Met His Pro Asp Arg Pro
325 330 335

Leu Val Ile Lys Thr Gly Val Gln Phe Thr Thr Lys Val Arg Leu Leu
340 345 350

Val Lys Phe Pro Glu Leu Asn Tyr Gln Leu Lys Ile Lys Val Cys Ile
355 360 365

Asp Lys Asp Ser Gly Asp Val Ala Ala Leu Arg Gly Ser Arg Lys Phe
370 375 380

Asn Ile Leu Gly Thr Asn Thr Lys Val Met Asn Met Glu Glu Ser Asn
385 390 395 400

Asn Gly Ser Leu Ser Ala Glu Phe Lys His Leu Thr Leu Arg Glu Gln
405 410 415

Arg Cys Gly Asn Gly Gly Arg Ala Asn Cys Asp Ala Ser Leu Ile Val
420 425 430

Thr Glu Glu Leu His Leu Ile Thr Phe Glu Thr Glu Val Tyr His Gln
435 440 445

Gly Leu Lys Ile Asp Leu Glu Thr His Ser Leu Pro Val Val Val Ile
450 455 460

Ser Asn Ile Cys Gln Met Pro Asn Ala Trp Ala Ser Ile Leu Trp Tyr
465 470 475 480

Asn Met Leu Thr Asn Asn Pro Lys Asn Val Asn Phe Phe Thr Lys Pro
485 490 495

Pro Ile Gly Thr Trp Asp Gln Val Ala Glu Val Leu Ser Trp Gln Phe
500 505 510

Ser Ser Thr Thr Lys Arg Gly Leu Ser Ile Glu Gln Leu Thr Thr Leu
515 520 525

Ala Glu Lys Leu Leu Gly Pro Gly Val Asn Tyr Ser Gly Cys Gln Ile
530 535 540

Thr Trp Ala Lys Phe Cys Lys Glu Asn Met Ala Gly Lys Gly Phe Ser
 545 550 555 560
 Phe Trp Val Trp Leu Asp Asn Ile Ile Asp Leu Val Lys Lys Tyr Ile
 565 570 575
 Leu Ala Leu Trp Asn Glu Gly Tyr Ile Met Gly Phe Ile Ser Lys Glu
 580 585 590
 Arg Glu Arg Ala Ile Leu Ser Thr Lys Pro Pro Gly Thr Phe Leu Leu
 595 600 605
 Arg Phe Ser Glu Ser Ser Lys Glu Gly Gly Val Thr Phe Thr Trp Val
 610 615 620
 Glu Lys Asp Ile Ser Gly Lys Thr Gln Ile Gln Ser Val Glu Pro Tyr
 625 630 635 640
 Thr Lys Gln Gln Leu Asn Asn Met Ser Phe Ala Glu Ile Ile Met Gly
 645 650 655
 Tyr Lys Ile Met Asp Ala Thr Asn Ile Leu Val Ser Pro Leu Val Tyr
 660 665 670
 Leu Tyr Pro Asp Ile Pro Lys Glu Glu Ala Phe Gly Lys Tyr Cys Arg
 675 680 685
 Pro Glu Ser Gln Glu His Pro Glu Ala Asp Pro Gly Ser Ala Ala Pro
 690 695 700
 Tyr Leu Lys Thr Lys Phe Ile Cys Val Thr Pro Thr Thr Cys Ser Asn
 705 710 715 720
 Thr Ile Asp Leu Pro Met Ser Pro Arg Thr Leu Asp Ser Leu Met Gln
 725 730 735
 Phe Gly Asn Asn Gly Glu Gly Ala Glu Pro Ser Ala Gly Gly Gln Phe
 740 745 750
 Glu Ser Leu Thr Phe Asp Met Asp Leu Thr Ser Glu Cys Ala Thr Ser
 755 760 765
 Pro Met
 770

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAYACNGARC CNATGGARAT YATT

24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAYGTNGAYC ARYTNAAAYAT G

21

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

RTCDATRTTN GRGTANAR

18

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTAYAANTYR AYCAGNGYAA

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATCGAGATG TATTTCAG AAAAG

25

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr Glu Leu Ile
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly Tyr Ile Lys Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys Val Asn Leu Gln Glu Arg Arg Lys Tyr Leu Lys His Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Glu Pro Gln Tyr Glu Glu Ile Pro Ile Tyr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Src
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Waksman, et al.

(C) JOURNAL: Nature
(D) VOLUME: 358
(F) PAGES: 646-653
(G) DATE: 1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg
1 5 10 15

Leu Leu Leu Asn Pro Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu
20 25 30

Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Phe
35 40 45

Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu
50 55 60

Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Ser Ser Leu
65 70 75 80

Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His
85 90 95

Arg Leu Thr Asn Val Cys Pro Thr Ser
100 105

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: Abl

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Overduin, et al.
(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
(D) VOLUME: 89
(F) PAGES: 11673-11677
(G) DATE: 1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu Lys His Ser Trp Tyr His Gly Pro Val Ser Arg Asn Ala Ala Glu
1 5 10 15

Tyr Leu Leu Ser Ser Gly Ile Asn Gly Ser Phe Leu Val Arg Glu Ser
20 25 30

Asp Arg Arg Pro Gly Gln Arg Ser Ile Ser Leu Arg Tyr Glu Glu Gly
35 40 45

Arg Val Tyr His Tyr Arg Ile Asn Thr Ala Ser Asp Gly Lys Leu Tyr
50 55 60

Val Ser Ser Glu Ser Arg Phe Asn Thr Leu Ala Glu Leu Val His His
65 70 75 80

His Ser Thr Val Ala Asp Gly Leu Ile Thr Thr Leu His Tyr Pro Ala
85 90 95

Pro Lys Arg

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:
(B) CLONE: Lck

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Eck, et al.
(C) JOURNAL: Nature
(D) VOLUME: 362
(F) PAGES: 87-91
(G) DATE: 1993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp Phe Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu
1 5 10 15

Ala Pro Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser
20 25 30

Thr Ala Gly Ser Phe Ser Leu Ser Val Arg Asp Asp Phe Asp Gln Asn
35 40 45

Gln Gly Glu Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly
50 55 60

Gly Phe Tyr Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Asp Leu
65 70 75 80

Val Arg His Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser
85 90 95

Arg Pro Cys Gln Thr Gln
100

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: p85[alpha]N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln Asp Ala Glu Trp Tyr Trp Gly Asp Ile Ser Arg Glu Glu Val Asn
1 5 10 15

Glu Lys Leu Arg Asp Thr Ala Asp Gly Thr Phe Leu Val Arg Asp Ala
20 25 30

Ser Thr Lys Met His Gly Asp Tyr Thr Leu Thr Leu Arg Lys Gly Gly
35 40 45

Asn Asn Lys Leu Ile Lys Ile Phe His Arg Asp Gly Lys Tyr Gly Phe
50 - 55 - 60

Ser Asp Pro Leu Thr Phe Asn Ser Val Val Glu Leu Ile Asn His Tyr
65 70 75 80

Arg His Glu Ser Leu Ala Gln Tyr Asn Pro Lys Leu Asp Val Lys Leu
85 90 95

Leu Tyr Pro